AMENDMENTS TO THE CLAIMS

Please amend the claims as follows.

1. (previously presented) A genetic testing method for systemic lupus erythematosus (SLE) in a human subject, comprising:

a) collecting a tissue sample from a human subject;

b) amplifying nucleic acids from said tissue sample to obtain amplification products, said nucleic acids comprising a genomic sequence of human chromosome 1 between microsatellite markers D1S2860 and D1S213; and

c) detecting in the amplification products the presence or absence of a twelve-fold CA dinucleotide repeat consisting of (SEQ. ID. NO.:6), wherein the presence of said twelve-fold CA dinucleotide repeat is diagnostic of SLE in a subject having SLE symptoms or indicates a genetic predisposition to develop SLE in a subject not presenting SLE symptoms.

2. (previously presented) The method of Claim 1, further comprising:

detecting in the amplification products the presence or absence of an eighteen-fold CA dinucleotide repeat consisting of (SEQ. ID. NO.:7), wherein the absence of said eighteen-fold CA dinucleotide repeat is diagnostic of SLE in subject having SLE symptoms or indicates a genetic predisposition to develop SLE in a subject not presenting SLE symptoms.

3. (previously presented) The method of Claim 1, wherein the tissue sample is a blood sample.

4. (previously presented) The method of Claim 1, wherein an oligonucleotide primer is used in amplifying said nucleic acids.

5. (previously presented) The method of Claim 4, wherein said primer has a nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, or AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long.

6. (previously presented) The method of Claim 4, wherein an oligonucleotide primer comprising nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.

7. (previously presented) The method of Claim 4, wherein an oligonucleotide primer comprising nucleotide sequence AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.

8. (previously presented) The method of Claim 4, wherein said oligonucleotide primer is labeled with a fluorescent dye.

9. (currently amended) The method of Claim 8, wherein said dye is selected from the group consisting of a cyclic-substituted unsymmetrical cyanine dye with Chemical Abstract Service Registry Number CAS 163795-75-3 (SYBR Green I), quinolinium,4-[(3-methyl-2(3H)-benzoxazolylidene) methyl]-1-[3-(triemthylammonio) propyl]-, diiodide (YO-PRO-1), 1,1'-(4,4,8,8-tetramethyl-4,8-diazaundecamethylene)-bis[4-[3-methyl-2,3-dihydro(benzo-1,3-thiazole)-2-methylidene]]quinolinium tetraiodide (thiazole orange), 6-carboxy-2',4'7',4,7-hexachlorofluorescein (Hex), 6-carboxyfluorescein (FAM) and~~or~~ 4,7,2',7'-tetrachloro-6-carboxyfluorescein (TET).

10-11. (canceled)

12. (previously presented) A genetic testing method for systemic lupus erythematosus (SLE) in a human subject, comprising:

a) collecting a tissue sample from a human subject;

b) amplifying nucleic acids from said tissue sample to obtain amplification products, said nucleic acids comprising a genomic sequence of human chromosome 1 between microsatellite markers D1S2860 and D1S213; and

c) detecting in the amplification products the presence or absence of an eighteen-fold CA dinucleotide repeat sequence consisting of (SEQ. ID. NO.:7), wherein the absence of said eighteen-fold CA dinucleotide repeat is diagnostic of SLE in a subject having SLE symptoms or indicates a genetic predisposition to develop SLE in a subject not presenting SLE symptoms.

13. (previously presented) The method of Claim 12, wherein the tissue sample is a blood sample.

14. (previously presented) The method of Claim 12, wherein an oligonucleotide primer is used in amplifying said nucleic acids.

15. (previously presented) The method of Claim 14, wherein said primer has a nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, or AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long.

16. (previously presented) The method of Claim 14, wherein an oligonucleotide primer comprising nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.

17. (previously presented) The method of Claim 14, wherein an oligonucleotide primer comprising nucleotide sequence AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.

18. (previously presented) The method of Claim 14, wherein said oligonucleotide primer is labeled with a fluorescent dye.

19. (currently amended) The method of Claim 18, wherein said dye is selected from the group consisting of a cyclic-substituted unsymmetrical cyanine dye with Chemical Abstract Service Registry Number CAS 163795-75-3 (SYBR Green I), quinolinium,4-[(3-methyl-2(3H)-benzoxazolylidene) methyl]-1-[3-(triemthylammonio) propyl]-, diiodide (YO-PRO-1), 1,1'-(4,4,8,8-tetramethyl-4,8-diazaundecamethylene)-bis[4-[3-methyl-2,3-dihydro(benzo-1,3-thiazole)-2-methylidene]]quinolinium tetraiodide (thiazole orange), 6-carboxy-2',4'7',4,7-hexachlorofluorescein (Hex), 6-carboxyfluorescein (FAM) and~~or~~ 4,7,2',7'-tetrachloro-6-carboxyfluorescein (TET).